

OIPÉ

Raw Sequence Listing Error Summary

**ERROR DETECTED**

**SUGGESTED CORRECTION**

SERIAL NUMBER: 09/911,132

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

- 1      Wrapped Nucleics  
    Wrapped Aminos      The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping."
- 2      Invalid Line Length      The rules require that a line not exceed 72 characters in length. This includes white spaces.
- 3      Misaligned Amino  
    Numbering      The numbering under each 5<sup>th</sup> amino acid is misaligned. Do not use tab codes between numbers; use space characters, instead.
- 4      Non-ASCII      The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text.
- 5      Variable Length      Sequence(s)      contain n's or Xaa's representing more than one residue. Per Sequence Rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.
- 6      PatentIn 2.0  
    "bug"      A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s)     . Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.
- 7      Skipped Sequences  
    (OLD RULES)      Sequence(s)      missing. If intentional, please insert the following lines for each skipped sequence:  
    (2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)  
    (i) SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)  
    (xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)  
    This sequence is intentionally skipped  
  
    Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.
- 8      Skipped Sequences  
    (NEW RULES)      Sequence(s)      missing. If intentional, please insert the following lines for each skipped sequence.  
    <210> sequence id number  
    <400> sequence id number  
    000
- 9      Use of n's or Xaa's  
    (NEW RULES)      Use of n's and/or Xaa's have been detected in the Sequence Listing.  
    Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present.  
    In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.
- 10      Invalid <213>  
    Response      Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or is Artificial Sequence
- 11 ✓ Use of <220>      Sequence(s)      ~~missing~~ <sup>most</sup> missing the <220> "Feature" and associated numeric identifiers and responses.  
    Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section.  
    (See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules)
- 12      PatentIn 2.0  
    "bug"      Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.
- 13      Misuse of n      n can only be used to represent a single nucleotide in a nucleic acid sequence. N is not used to represent any value not specifically a nucleotide.

0570  
0906

#13



OIPE

ENTERED

## RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/911,132A

DATE: 09/09/2002

TIME: 09:38:01

Input Set : A:\RDID 0073US-2.ST25.txt

Output Set: N:\CRF4\09092002\I911132A.raw

3 <110> APPLICANT: Roche Diagnostics GmbH  
 5 <120> TITLE OF INVENTION: Expression of Alkaline Phosphatase in Yeast  
 7 <130> FILE REFERENCE: RDID 0073US  
 9 <140> CURRENT APPLICATION NUMBER: 09/911,132A  
 C--> 10 <141> CURRENT FILING DATE: 2002-08-28  
 12 <160> NUMBER OF SEQ ID NOS: 38  
 14 <170> SOFTWARE: PatentIn version 3.1  
 16 <210> SEQ ID NO: 1  
 17 <211> LENGTH: 1476  
 18 <212> TYPE: DNA  
 19 <213> ORGANISM: Bovine  
 21 <400> SEQUENCE: 1  
 22 gaattcctca tcccagctga ggaggaaaac cccgccttct ggaaccgcca ggcagcccag 60  
 24 gcccttgatg tagccaagaa gttgcagccg atccagacag ctgccaagaa tgtcatcctc 120  
 26 ttcttggggg atgggatggg ggtgcctacg gtgacagcca ctcgatcct aaaggggcag 180  
 28 atgaatggca aactgggacc tgagacaccc ctggccatgg accagttccc atacgtggct 240  
 30 ctgtccaaga catacaacgt ggacagacag gtgccagaca gcgcaggcac tgccactgcc 300  
 32 tacctgtgtg ggggtcaagg caactacaga accatcggtg taagtgcagc cgcccgtac 360  
 34 aatcagtga acacgacacg tgggaatgag gtcacgtctg tgatcaaccg ggccaagaaa 420  
 36 gcaggggaagg ccgtgggagt ggtgaccacc accaggggtg agcatgcctc cccagccggg 480  
 38 gcctacgcgc acacggtgaa ccgaaactgg tactcagacg ccgacctgcc tgctgatgca 540  
 40 cagaagaatg gctgccagga catcgccgca cagctggtct acaacatgga tattgacgtg 600  
 42 atcctgggtg gaggccgaat gtacatgttt cctgagggga cccagaccc tgaataccca 660  
 44 gatgatgcca gtgtgaatgg agtccggaag gacaagcaga acctggtgca ggaatggcag 720  
 46 gccaagcacc agggagccca gtatgtgtgg aaccgcactg cgctccttca ggcggccgat 780  
 48 gactccagtg taacacacct catgggcctc tttgagccgg cagacatgaa gtataatgtt 840  
 50 cagcaagacc acaccaagga cccgaccctg gcggagatga cggaggcggc cctgcaagtg 900  
 52 ctgagcagga acccccggg cttctacctc ttctgtggagg gaggccgcat tgaccacggt 960  
 54 caccatgacg gcaaagctta tatggcactg actgaggcga tcatgtttga caatgccatc 1020  
 56 gccaaggcta acgagctcac tagcgaactg gacacgctga tccttgctac tgcagaccac 1080  
 58 tcccatgtct tctcttttgg tggctacaca ctgcgtggga cctccatttt cggctctggc 1140  
 60 ccgggcaagg ccttagacag caagtcctac acctccatcc tctatggcaa tggcccaggc 1200  
 62 tatgcgcttg gcgggggctc gagggccgat gttaatggca gcacaagcga ggaaccctca 1260  
 64 taccggcagc aggcgggccgt gccctggct agcgagaccc acgggggcga agacgtggcg 1320  
 66 gtgttcgcgc gagggccgca ggcgcacctg gtgcacggcg tgcaggagga gaccttcgtg 1380  
 68 gcgcacatca tggcctttgc gggctgcgtg gagccctaca ccgactgcaa tctgccagcc 1440  
 70 cccgccaccg ccaccagcat ccccgactag ggtacc 1476  
 73 <210> SEQ ID NO: 2  
 74 <211> LENGTH: 40  
 75 <212> TYPE: DNA  
 76 <213> ORGANISM: Artificial Sequence  
 78 <220> FEATURE:  
 79 <223> OTHER INFORMATION: Primer

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81 <400> SEQUENCE: 2
82 gcgcgaattc ctcatcccag ctgaggagga aaaccccgcc 40
85 <210> SEQ ID NO: 3
86 <211> LENGTH: 36
87 <212> TYPE: DNA
88 <213> ORGANISM: Artificial Sequence
90 <220> FEATURE:
91 <223> OTHER INFORMATION: Primer
93 <400> SEQUENCE: 3
94 cgcgggtacc ctatgcgggg atgctggtgg cggtgg 36
97 <210> SEQ ID NO: 4
98 <211> LENGTH: 487
99 <212> TYPE: PRT
100 <213> ORGANISM: Bovine
102 <400> SEQUENCE: 4
104 Leu Ile Pro Ala Glu Glu Glu Asn Pro Ala Phe Trp Asn Arg Gln Ala
105 1 5 10 15
108 Ala Gln Ala Leu Asp Val Ala Lys Lys Leu Gln Pro Ile Gln Thr Ala
109 20 25 30
112 Ala Lys Asn Val Ile Leu Phe Leu Gly Asp Gly Met Gly Val Pro Thr
113 35 40 45
116 Val Thr Ala Thr Arg Ile Leu Lys Gly Gln Met Asn Gly Lys Leu Gly
117 50 55 60
120 Pro Glu Thr Pro Leu Ala Met Asp Gln Phe Pro Tyr Val Ala Leu Ser
121 65 70 75 80
124 Lys Thr Tyr Asn Val Asp Arg Gln Val Pro Asp Ser Ala Gly Thr Ala
125 85 90 95
128 Thr Ala Tyr Leu Cys Gly Val Lys Gly Asn Tyr Arg Thr Ile Gly Val
129 100 105 110
132 Ser Ala Ala Ala Arg Tyr Asn Gln Cys Asn Thr Thr Arg Gly Asn Glu
133 115 120 125
136 Val Thr Ser Val Ile Asn Arg Ala Lys Lys Ala Gly Lys Ala Val Gly
137 130 135 140
140 Val Val Thr Thr Thr Arg Val Gln His Ala Ser Pro Ala Gly Ala Tyr
141 145 150 155 160
144 Ala His Thr Val Asn Arg Asn Trp Tyr Ser Asp Ala Asp Leu Pro Ala
145 165 170 175
148 Asp Ala Gln Lys Asn Gly Cys Gln Asp Ile Ala Ala Gln Leu Val Tyr
149 180 185 190
152 Asn Met Asp Ile Asp Val Ile Leu Gly Gly Gly Arg Met Tyr Met Phe
153 195 200 205
156 Pro Glu Gly Thr Pro Asp Pro Glu Tyr Pro Asp Asp Ala Ser Val Asn
157 210 215 220
160 Gly Val Arg Lys Asp Lys Gln Asn Leu Val Gln Glu Trp Gln Ala Lys
161 225 230 235 240
164 His Gln Gly Ala Gln Tyr Val Trp Asn Arg Thr Ala Leu Leu Gln Ala
165 245 250 255
168 Ala Asp Asp Ser Ser Val Thr His Leu Met Gly Leu Phe Glu Pro Ala
169 260 265 270

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172 Asp Met Lys Tyr Asn Val Gln Gln Asp His Thr Lys Asp Pro Thr Leu
173          275          280          285
176 Ala Glu Met Thr Glu Ala Ala Leu Gln Val Leu Ser Arg Asn Pro Arg
177          290          295          300
180 Gly Phe Tyr Leu Phe Val Glu Gly Gly Arg Ile Asp His Gly His His
181 305          310          315          320
184 Asp Gly Lys Ala Tyr Met Ala Leu Thr Glu Ala Ile Met Phe Asp Asn
185          325          330          335
188 Ala Ile Ala Lys Ala Asn Glu Leu Thr Ser Glu Leu Asp Thr Leu Ile
189          340          345          350
192 Leu Val Thr Ala Asp His Ser His Val Phe Ser Phe Gly Gly Tyr Thr
193          355          360          365
196 Leu Arg Gly Thr Ser Ile Phe Gly Leu Ala Pro Gly Lys Ala Leu Asp
197          370          375          380
200 Ser Lys Ser Tyr Thr Ser Ile Leu Tyr Gly Asn Gly Pro Gly Tyr Ala
201 385          390          395          400
204 Leu Gly Gly Gly Ser Arg Pro Asp Val Asn Gly Ser Thr Ser Glu Glu
205          405          410          415
208 Pro Ser Tyr Arg Gln Gln Ala Ala Val Pro Leu Ala Ser Glu Thr His
209          420          425          430
212 Gly Gly Glu Asp Val Ala Val Phe Ala Arg Gly Pro Gln Ala His Leu
213          435          440          445
216 Val His Gly Val Gln Glu Glu Thr Phe Val Ala His Ile Met Ala Phe
217          450          455          460
220 Ala Gly Cys Val Glu Pro Tyr Thr Asp Cys Asn Leu Pro Ala Pro Ala
221 465          470          475          480
224 Thr Ala Thr Ser Ile Pro Asp
225          485

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228 &lt;210&gt; SEQ ID NO: 5

229 &lt;211&gt; LENGTH: 1476

230 &lt;212&gt; TYPE: DNA

231 &lt;213&gt; ORGANISM: Artificial Sequence

233 &lt;220&gt; FEATURE:

234 &lt;223&gt; OTHER INFORMATION: Codon-optimized DNA sequence

236 &lt;400&gt; SEQUENCE: 5

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237 gaattcttga ttccagctga agaagaaaat ccagcttttt ggaatagaca agctgctcaa      60
239 gctttggatg ttgctaagaa gttgcaacca attcaaactg ctgctaagaa tgttattttg      120
241 tttttgggtg atggtatggg tgttccaact gttactgcta ctagaatttt gaaggggtcaa      180
243 atgaatggta agttgggtcc agaaactcca ttggctatgg atcaatttcc atacgttgct      240
245 ttgtctaaga cttacaatgt tgatagacaa gttccagatt ctgctgggtac tgctactgct      300
247 tacttgtgtg gtgttaaggg taattacaga actattgggtg tttctgctgc tgctagatac      360
249 aatcaatgta atactactag aggtaatgaa gttacttctg ttattaatag agctaagaag      420
251 gctggtaagg ctgttggtgt tgttactact actagagttc aacatgcttc tccagctggt      480
253 gcttacgctc atactgttaa tagaaattgg tactctgatg ctgatttgcc agctgatgct      540
255 caaagaatg gttgtcaaga tattgctgct caattggttt acaatatgga tattgatggt      600
257 attttgggtg gtggtagaat gtacatgttt ccagaaggta ctccagatcc agaataccca      660
259 gatgatgctt ctgttaatgg tgttagaaag gataagcaaa atttggttca agaatggcaa      720
261 gctaagcatc aaggtgctca atatgttttg aatagaactg ctttgttgca agctgctgat      780
263 gattctagtg ttactcattt gatgggtttg tttgaaccag ctgatatgaa gtataatggt      840

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265 caacaagatc atactaagga tccaactttg gctgaaatga ctgaagctgc tttgcaagtt      900
267 ttgtctagaa atccaagagg tttttacttg tttgttgaag gtggtagaat tgatcatggt      960
269 catcatgatg gtaaggctta tatggctttg actgaagcta ttatgtttga taatgctatt     1020
271 gctaaggcta atgaattgac ttctgaattg gatactttga ttttggttac tgctgatcat     1080
273 agtcatgttt tttcttttgg tggttacact ttgagaggta cttctatatt tggtttggct     1140
275 ccaggtaagg ctttgatag taagtcttac acttctatatt tgtatggtaa tgggccaggt     1200
277 tatgctttgg gtggtggttc tagaccagat gttaatggta gtactagtga agaaccatct     1260
279 tacagacaac aagctgctgt tccattggct agtgaaactc atggtggtga agatgttgct     1320
281 gttttttgcta gaggtccaca agctcatttg gttcatgggt ttcaagaaga aacttttggt     1380
283 gctcatatta tggcttttgc tggttgtgtt gaaccataca ctgattgtaa tttgccagct     1440
285 ccagctactg ctactagtat tccagattaa ggtacc                                1476
288 <210> SEQ ID NO: 6
289 <211> LENGTH: 78
290 <212> TYPE: DNA
291 <213> ORGANISM: Artificial Sequence
293 <220> FEATURE:
294 <223> OTHER INFORMATION: Primer
296 <400> SEQUENCE: 6
297 gcgcgaattc ttgattccag ctgaagaaga aaatccagct ttttgaata gacaagctgc      60
299 tcaagctttg gatgttgc                                78
302 <210> SEQ ID NO: 7
303 <211> LENGTH: 70
304 <212> TYPE: DNA
305 <213> ORGANISM: Artificial Sequence
307 <220> FEATURE:
308 <223> OTHER INFORMATION: Primer
310 <400> SEQUENCE: 7
311 ccaaaaacaa aataacattc ttagcagcag tttgaattgg ttgcaacttc ttagcaacat      60
313 ccaaagcttg                                70
316 <210> SEQ ID NO: 8
317 <211> LENGTH: 69
318 <212> TYPE: DNA
319 <213> ORGANISM: Artificial Sequence
321 <220> FEATURE:
322 <223> OTHER INFORMATION: Primer
324 <400> SEQUENCE: 8
325 gaatgttatt ttgtttttgg gtgatgggat ggggtgtcca actgttactg ctactagaat      60
327 tttgaaggg                                69
330 <210> SEQ ID NO: 9
331 <211> LENGTH: 70
332 <212> TYPE: DNA
333 <213> ORGANISM: Artificial Sequence
335 <220> FEATURE:
336 <223> OTHER INFORMATION: Primer
338 <400> SEQUENCE: 9
339 ggaaattgat ccatagccaa tggagtttct ggaccaact taccattcat ttgacccttc      60
341 aaaattctag                                70
344 <210> SEQ ID NO: 10
345 <211> LENGTH: 71

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## RAW SEQUENCE LISTING

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Input Set : A:\RDID 0073US-2.ST25.txt

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346 <212> TYPE: DNA
347 <213> ORGANISM: Artificial Sequence
349 <220> FEATURE:
350 <223> OTHER INFORMATION: Primer
352 <400> SEQUENCE: 10
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355 ccagattctg c                                                                71
358 <210> SEQ ID NO: 11
359 <211> LENGTH: 71
360 <212> TYPE: DNA
361 <213> ORGANISM: Artificial Sequence
363 <220> FEATURE:
364 <223> OTHER INFORMATION: Primer
366 <400> SEQUENCE: 11
367 ccaatagttc tgtaattacc cttaacacca cacaagtaag cagtagcagt accagcagaa      60
369 tctggaactt g                                                                71
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373 <211> LENGTH: 72
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375 <213> ORGANISM: Artificial Sequence
377 <220> FEATURE:
378 <223> OTHER INFORMATION: Primer
380 <400> SEQUENCE: 12
381 gtaattacag aactattggt gtttctgctg ctgctagata caatcaatgt aatactacta      60
383 gaggtaatga ag                                                                72
386 <210> SEQ ID NO: 13
387 <211> LENGTH: 74
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389 <213> ORGANISM: Artificial Sequence
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392 <223> OTHER INFORMATION: Primer
394 <400> SEQUENCE: 13
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397 attacctcta gtag                                                                74
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401 <211> LENGTH: 74
402 <212> TYPE: DNA
403 <213> ORGANISM: Artificial Sequence
405 <220> FEATURE:
406 <223> OTHER INFORMATION: Primer
408 <400> SEQUENCE: 14
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411 catactgtta atag                                                                74
414 <210> SEQ ID NO: 15
415 <211> LENGTH: 68
416 <212> TYPE: DNA
417 <213> ORGANISM: Artificial Sequence
419 <220> FEATURE:
420 <223> OTHER INFORMATION: Primer

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VERIFICATION SUMMARY

DATE: 09/09/2002

PATENT APPLICATION: US/09/911,132A

TIME: 09:38:02

Input Set : A:\RDID 0073US-2.ST25.txt

Output Set: N:\CRF4\09092002\I911132A.raw

L:10 M:271 C: Current Filing Date differs, Replaced Current Filing Date